



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket: KONGERSLEV1

In re Application of:) Conf. No.: 6668
Leif KONGERSLEV)
) Washington, D.C.
)
U.S. Appln. No.:)
10/820,155) July 23, 2004
)
For: TREATMENT OF SARS IN...)

RESPONSE TO "SEQUENCE LISTING" REQUIREMENT

Honorable Commissioner for Patents
U.S. Patent and Trademark Office
2011 South Clark Place
Customer Window, **Mail Stop Sequence**
Crystal Plaza Two, Lobby, Room 1B03
Arlington, Virginia 22202

Sir:

This paper is filed in response to the Notification
of Defective Response, mailed March 1, 2004.

1. Applicants hereby submit the following:

a paper copy of a "Sequence Listing", complying
with §1.821(c), to be incorporated into the
specification as directed above;

an amendment to the paper copy of the "Sequence
Listing" submitted on -----, the
amendment being in the form of substitute
sheets;

the Sequence Listing in computer readable form,
complying with §1.821(e) and §1.824, including,

if an amendment to the paper copy is submitted,
all previously submitted data with the
amendment incorporated therein;

[] a substitute computer readable form to replace
one found to be damaged or unreadable.

[] The computer readable form in this application
no. 09/... is identical with that filed on
[date sequence was filed] in application no. 09/
, filed [filing date]. In accordance with 37
C.F.R. §1.821(e), please use the [first-filed,
last-filed or only, whichever is applicable]
computer readable form filed in that application
as the computer readable form for the instant
application. It is understood that the Patent
and Trademark Office will make the necessary
change in application number and filing date for
the instant application. A paper copy of the
Sequence Listing is [included in the originally-
filed specification of the instant application,
included in a separately filed preliminary
amendment for incorporation into the
specification, whichever is applicable].

2. The description has been amended to comply with
§1.821(d).

3. The undersigned attorney or agent hereby states as follows:

- (a) this submission does not include new matter [§1.821(g)];
- (b) the contents of the paper copy (as amended, if applicable) and the computer readable form of the Sequence Listing, are the same [§1.821(f) and §1.825(b)];
- (c) if the paper copy has been amended, the amendment is supported by the specification and does not include new matter [§1.825(a)]; and
- (d) if the computer readable form submitted herewith is a substitute for a form found upon receipt by the PTO to be damaged or unreadable, that the substitute data is identical to that originally intended to be filed [§1.825(d)].

4. Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence

and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

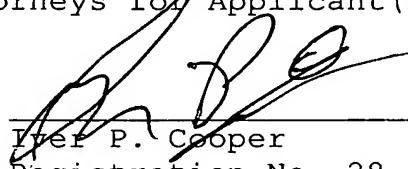
The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the

results of his or her sequence search against a database containing known natural sequences.

Respectfully submitted,

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